re-run

RAW SEQUENCE LISTING PATENT APPLICATION: **US/10/533,037**	DATE: 07/20/2006 TIME: 19:15:29

Input Set : **N:\Crf4\Refhold\10_folder\J533037.raw**
Output Set: **N:\CRF4\07202006\J533037.raw**

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 1 <110> APPLICANT: Chang, Chawnshang
 2       Yi-Fen Lee
 3       Wen-Jye Lin
 4 <120> TITLE OF INVENTION: Hydroxyflutamide Induced Pathways
 5       Related to Androgen Receptor Negative Prostate Cancer Cells
 6 <130> FILE REFERENCE: 21108.0017U2
 7 <140> CURRENT APPLICATION NUMBER: US/10/533,037
 8 <141> CURRENT FILING DATE: 2005-04-28
 9 <150> PRIOR APPLICATION NUMBER: PCT/US03/34636
10 <151> PRIOR FILING DATE: 2003-10-31
11 <150> PRIOR APPLICATION NUMBER: 60/423,340
12 <151> PRIOR FILING DATE: 2002-10-31
13 <160> NUMBER OF SEQ ID NOS: 28
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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17 <211> LENGTH: 1587
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
20 <220> FEATURE:
21 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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26       ctgaaagtcc atctgctgca tcggtcaaga gaaactccac ttgcatgaag attgcacgcc     180
27       tgcagcttgc atctttgttg caaaactagc tacagaagag aagcaaggca aagtcttttg     240
28       tgctcccctc ccccatcaaa ggaaggggga aaatgtctca gtcgaaaggc aagaagcgaa     300
29       accctggcct taaaattcca aaagaagcat ttgaacaacc tcagaccagt tccacaccac     360
30       ctagagattt agactccaag gcttgcattt ctattggaaa tcagaacttt gaggtgaagg     420
31       cagatgacct ggagcctata atggaactgg gacgaggtgc gtacggggtg gtggagaaga     480
32       tgcggcacgt gcccagcggg cagatcatgg cagtgaagcg gatccgagcc acagtaaata     540
33       gccaggaaca gaaacggcta ctgatggatt tggatatttc catgaggacg gtggactgtc     600
34       cattcactgt caccttttat ggcgcactgt ttcgggaggg tgatgtgtgg atctgcatgg     660
35       agctcatgga tacatcacta gataaattct acaaacaagt tattgataaa ggccagacaa     720
36       ttccagagga catcttaggg aaaatagcag tttctattgt aaaagcatta gaacatttac     780
37       atagtaagct gtctgtcatt cacagagacg tcaagccttc taatgtactc atcaatgctc     840
38       tcggtcaagt gaagatgtgc gattttggaa tcagtggcta cttggtggac tctgttgcta     900
39       aaacaattga tgcaggttgc aaaccataca tggcccctga agaataaac ccagagctca     960
40       accagaaggg atacagtgtg aagtctgaca tttggagtct gggcatcacg atgattgagt    1020
41       tggccatcct tcgatttccc tatgattcat ggggaactcc atttcagcag ctcaaacagg    1080
42       tggtagagga gccatcgcca caactcccag cagacaagtt ctctgcagag tttgttgact    1140
43       ttacctcaca gtgcttaaag aagaattcca aagaacggcc tacataccca gagctaatgc    1200
44       aacatccatt tttcacccta catgaatcca aaggaacaga tgtggcatct tttgtaaaac    1260
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45      tgattcttgg agactaaaaa gcagtggact taatcggttg accctactgt ggattggtgg      1320
46      gtttcggggt gaagcaagtt cactacagca tcaatagaaa gtcatctttg agataattta      1380
47      accctgcctc tcagagggtt ttctctccca attttctttt tactccccct cttaagggggg     1440
48      ccttggaatc tatagtatag aatgaactgt ctagatggat gaattatgat aaaggcttag      1500
49      gacttcaaaa ggtgattaaa tatttaatga tgtgtcatat gaaaaaaaaa aaaaaaaaaa      1560
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56 <220> FEATURE:
57 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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62      Lys Glu Ala Phe Glu Gln Pro Gln Thr Ser Ser Thr Pro Pro Arg Asp
63                   20                  25                  30
64      Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu Val
65                   35                  40                  45
66      Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala Tyr
67           50                  55                  60
68      Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met Ala
69       65                  70                  75                  80
70      Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg Leu
71                   85                  90                  95
72      Leu Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe Thr
73                   100                 105                 110
74      Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile Cys
75                   115                 120                 125
76      Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val Ile
77                   130                 135                 140
78      Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala Val
79      145                 150                 155                 160
80      Ser Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val Ile
81                   165                 170                 175
82      His Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly Gln
83                   180                 185                 190
84      Val Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser Val
85                   195                 200                 205
86      Ala Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu Arg
87           210                 215                 220
88      Ile Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp Ile
89      225                 230                 235                 240
90      Trp Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe Pro
91                   245                 250                 255
92      Tyr Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val Glu
93                   260                 265                 270
94      Glu Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe Val
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Output Set: **N:\CRF4\07202006\J533037.raw**

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 96       Asp Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro Thr
 97           290                  295                  300
 98       Tyr Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser Lys
 99       305               310                  315                  320
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101                     325                  330
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106 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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113       gctactgaca gcttctcagg caggttcgaa gatgtctatc agctgcagga ggatgtgctg     180
114       ggggaaggtg ctcacgctcg tgtgcagacc tgtgtcaatc tcatcaccaa ccaggaatat     240
115       gctgtcaaga tcattgagaa gcagctgggc cacatccgca gcagggtgtt ccgggaggtg     300
116       gagatgctgt accagtgcca gggacatagg aatgttctag aactgattga gttctttgag     360
117       gaggaggacc gtttctacct ggtgtttgag aagatgcgtg gcggatccat cctaagccac     420
118       atccatagaa ggcgccactt taacgagctg gaggccagcg tggtagtaca ggacgtggcc     480
119       agtgccctgg acttcctgca taacaaaggc atcgcccaca gggacctaaa gccagagaac     540
120       atcctatgtg agcaccccaa ccaggtctcg ccagtgaaga tctgcgactt cgaccttggc     600
121       agtggtatca aactcaatgg agactgctcc cccatctcca caccagagct gctcacccccg     660
122       tgtgggtcag ctgagtacat ggccccagag gtggtggagg ccttcagtga agaggccagc     720
123       atctacgaca agcgctgcga cctgtggagc ctgggcgtca tcctctacat cctgcttagt     780
124       ggctacccgc ccttcgtggg ccactgtggc agcgactgtg gctgggaccg tggggaggcc     840
125       tgtcctgcct gccagaacat gctgtttgag agcatccagg agggcaagta tgagttccct     900
126       gacaaggact ggtcccacat ctcctttgct gccaaagacc tcatctccaa gctgctggtc     960
127       cgagatgcca agcagaggct gagtgctgcc caagtcctgc agcatccctg ggtgcagggg    1020
128       tgtgccccag agaacaccct accgacaccc ttggttctgc agaggaacag ctgtgccaaa    1080
129       gacctcacgt cctttgcggc tgaggccatc gccatgaacc ggcagctggc ccagtgtgag    1140
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131       tccccaccct cccagtccaa gctggcccag cggcgccaga gggctagcct gtcggccacc    1260
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133       gccccgcggg gcctgaaggc tagggacctg gacaccccac cccttgccat tccaggtgcc    1380
134       agctcagctg ggtcctctgg gggtgtaggg gtctgttagg gggtgtctcc ttttctccct    1440
135       gtccttcccc tgccctgccc acttggcttt gttttgtttg tttttctttg ccgctattga    1500
136       aagcaagtgc ccggaggagg gcggagggct caggccgccc agcctgcacc ccacgatgct    1560
137       cacctgccaa ctgtgaaggt cctgccacct gcgcccccac ctccactcca gccactctgc    1620
138       tgtcttccag ggttggggat cccgcagggt cagcacccca cacctctccc agccctcagt    1680
139       gttgtcaggg acaggccctc ctggtgagca cagtggtggt tgcatctcct caccagagca    1740
140       cccttgggtc tggggtaggg cagggctccc tgtcttggat agagacctct ggggagcagg    1800
141       tggatgggga cagtgcactt gattgacccc gagtccccat catccacctg cagtgtccct    1860
142       tggagggttg acaatcagaa acccctccca ggctgcttag ctccttgccc tgggacagac    1920
143       ctactgctcc caaccccact tcccaggggc agagctggaa ggggaccctg cacccagcta    1980
144       gctccaccac agcaggagag gtgctggacc aggctttcat cagcaaacat ggggctccca    2040
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145      catgtctccc cacccagggc acctgagtgc cccttctcag ggctcagcct gaccacggcc    2100
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147      catacccagg gctctcacct tcctgttgcc cccagagggc agcagctcag gcgtgcctgc    2220
148      tttcaggaaa gggaggctgg gaagggatgt ggtggccctg cggtgcccag acctaactgc    2280
149      ccgaggcctg tagactgttc tagccgaact actatgcaat acaagttccc attttctcca    2340
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151      ggtgtctaca gggcagcccc tggcctcaaa aatccttggt caggattgtt tgtcgagttt    2460
152      agtttaggct ttttttttt tttaaagaa ataatttgac ttgcttccct gttcttgaag      2520
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154      ccaccctcct ccctagtctc ataggatcgt cacagtggag gtgacatgcc ttctccagtc    2640
155      ctgccccacc tgcctctgtg dacacatttc caaagaaccc ctgggggtgg gacctcctcc    2700
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157      aacctgactg ggcagtgagc agcattgacc cccactcacc cccaaaacag ggctgtgatt    2820
158      tccttagtcc ttccaagccc gacctggagg atgggtcaga ccccttaact gtgaatgaga    2880
159      catgatcctg ggctggcttc gccacaaacc atgcagaaat ctaaaaggcc tgttgtagag    2940
160      tgggggacat gcaagcactt ttaactccat cgtaccaggt gaactgacct ccggactcct    3000
161      ttcccaccaa ctgtcaacgc caggattttg tattctgttt tgtaaggatt taataaaagt    3060
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164 <210> SEQ ID NO: 4
165 <211> LENGTH: 412
166 <212> TYPE: PRT
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169 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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174   Arg Lys Lys Lys Arg Cys Arg Ala Thr Asp Ser Phe Ser Gly Arg Phe
175   20   25   30
176   Glu Asp Val Tyr Gln Leu Gln Glu Asp Val Leu Gly Glu Gly Ala His
177   35   40   45
178   Ala Arg Val Gln Thr Cys Val Asn Leu Ile Thr Asn Gln Glu Tyr Ala
179   50   55   60
180   Val Lys Ile Ile Glu Lys Gln Leu Gly His Ile Arg Ser Arg Val Phe
181   65   70   75   80
182   Arg Glu Val Glu Met Leu Tyr Gln Cys Gln Gly His Arg Asn Val Leu
183   85   90   95
184   Glu Leu Ile Glu Phe Phe Glu Glu Asp Arg Phe Tyr Leu Val Phe
185   100   105   110
186   Glu Lys Met Arg Gly Gly Ser Ile Leu Ser His Ile His Arg Arg Arg
187   115   120   125
188   His Phe Asn Glu Leu Glu Ala Ser Val Val Val Gln Asp Val Ala Ser
189   130   135   140
190   Ala Leu Asp Phe Leu His Asn Lys Gly Ile Ala His Arg Asp Leu Lys
191   145   150   155   160
192   Pro Glu Asn Ile Leu Cys Glu His Pro Asn Gln Val Ser Pro Val Lys
193   165   170   175
194   Ile Cys Asp Phe Asp Leu Gly Ser Gly Ile Lys Leu Asn Gly Asp Cys

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195                    180                185                190
196      Ser Pro Ile Ser Thr Pro Glu Leu Leu Thr Pro Cys Gly Ser Ala Glu
197              195                200                205
198      Tyr Met Ala Pro Glu Val Val Glu Ala Phe Ser Glu Glu Ala Ser Ile
199              210                215                220
200      Tyr Asp Lys Arg Cys Asp Leu Trp Ser Leu Gly Val Ile Leu Tyr Ile
201      225                230                235                240
202      Leu Leu Ser Gly Tyr Pro Pro Phe Val Gly His Cys Gly Ser Asp Cys
203              245                250                255
204      Gly Trp Asp Arg Gly Glu Ala Cys Pro Ala Cys Gln Asn Met Leu Phe
205              260                265                270
206      Glu Ser Ile Gln Glu Gly Lys Tyr Glu Phe Pro Asp Lys Asp Trp Ser
207              275                280                285
208      His Ile Ser Phe Ala Ala Lys Asp Leu Ile Ser Lys Leu Leu Val Arg
209              290                295                300
210      Asp Ala Lys Gln Arg Leu Ser Ala Ala Gln Val Leu Gln His Pro Trp
211      305                310                315                320
212      Val Gln Gly Cys Ala Pro Glu Asn Thr Leu Pro Thr Pro Leu Val Leu
213              325                330                335
214      Gln Arg Asn Ser Cys Ala Lys Asp Leu Thr Ser Phe Ala Ala Glu Ala
215              340                345                350
216      Ile Ala Met Asn Arg Gln Leu Ala Gln Cys Glu Glu Asp Ala Gly Gln
217              355                360                365
218      Asp Gln Pro Val Val Ile Arg Ala Thr Ser Arg Cys Leu Gln Leu Ser
219              370                375                380
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225 <210> SEQ ID NO: 5
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243      cgcctagtgc tgactccact cctgacgtaa accagtctcc tcggggcaaa cgtagggcaa     660
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